

FIG. 1

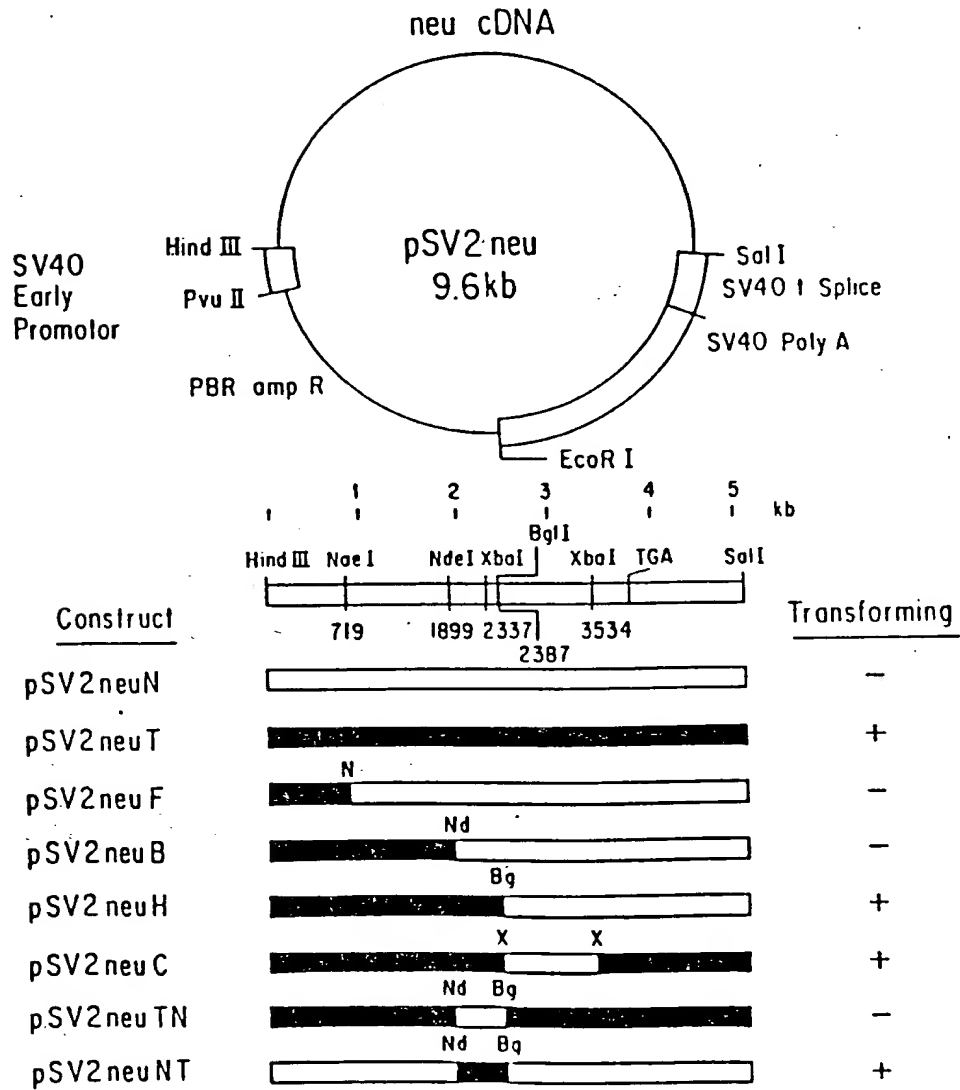


FIG.3

normal

glu	gln	arg	ala	ser	pro	val	thr	phe	ile	ile	ala	thr	val	:	gly	val
GAG	CAG	AGA	GCC	AGC	CCG	GTG	ACA	TTC	ATC	ATT	GCA	ACT	GTA	:	GGC	CTC

aa 666

transforming

val
GTC
:
:
GAG
glu

leu	leu	phe	leu	ile	leu	val	val	val	val	gly	ile	leu	ile	lys	arg	arg
CTG	CTG	TTC	CTG	ATC	TTA	GTG	GTG	GTG	GTT	GGA	ATC	CTA	ATC	AAA	CGA	AGG

aa 683

FIG. 4

A) ACGCCCACTACAGTTGCAAT

nucleotides 1999-2018, wild-type sequence

*

B) ACGCCCTCTACAGTTGCAAT

nucleotides 999-2018, T₂₀₁₂ to A

G) CCGTCCTCAGCTGTGACC

nucleotides 996-1013, control probe

*

D) ACGCCCCCTACAGTTGCAAT

nucleotides 1999-2018, T₂₀₁₂ to G

FIG.5

a b c d e f



a b c d e f

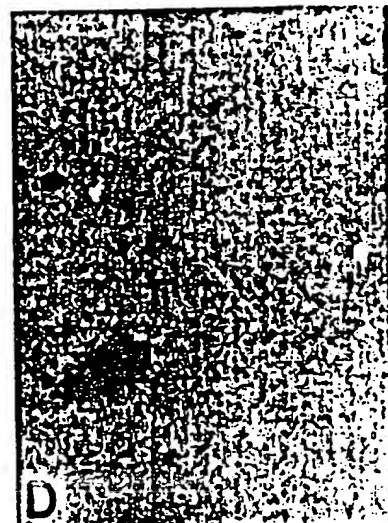
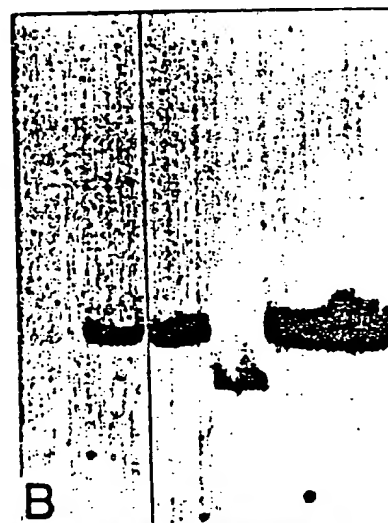


FIG. 6

a b c d e f g h i j

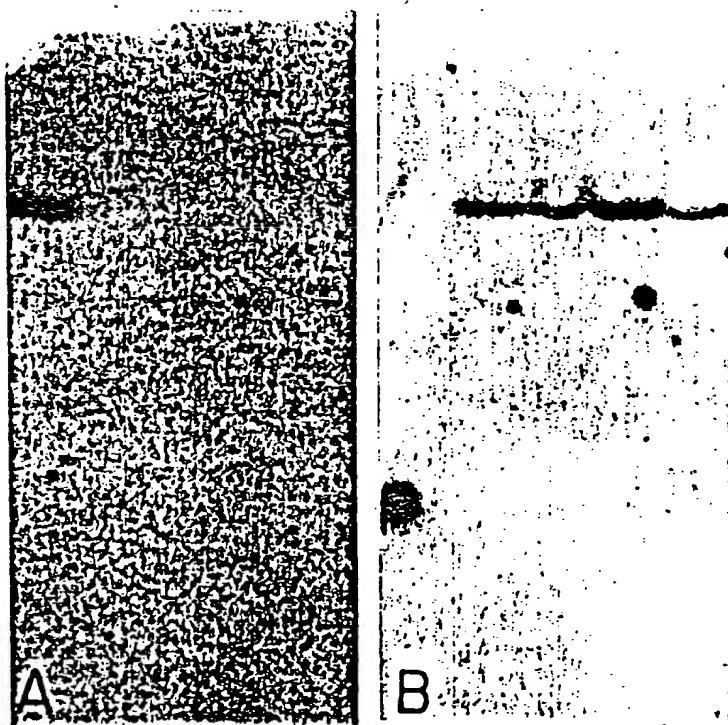
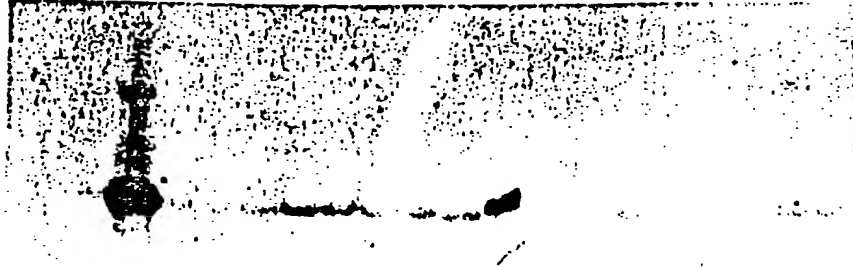
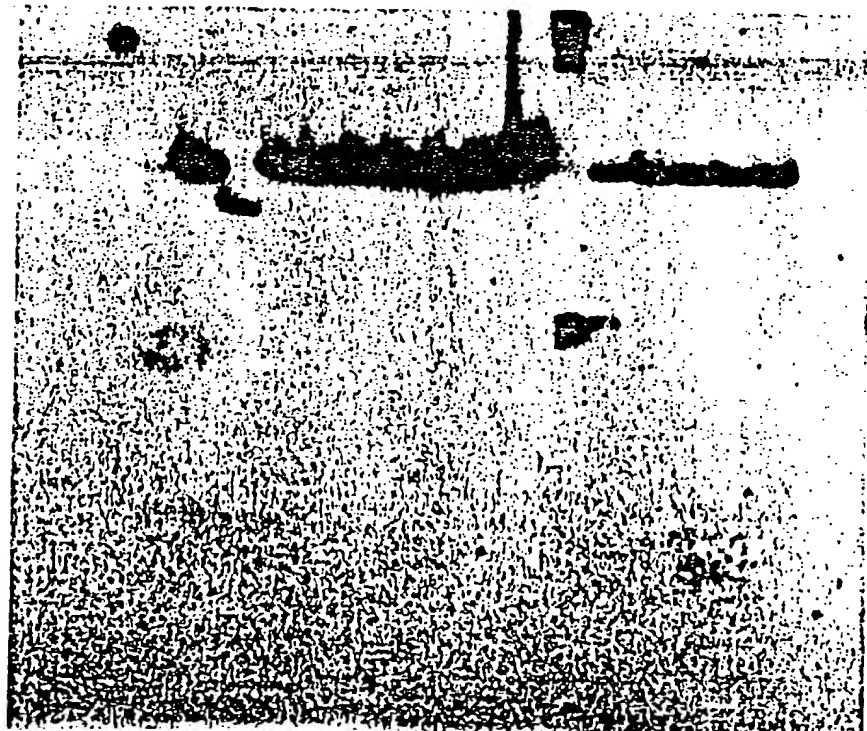


FIG.7

N G B 1 2 3 4 5 6 7 8 9 10 11 12 13 14 cl c2



N G B 1 2 3 4 5 6 7 8 9 10 11 12 13 14 cl c2



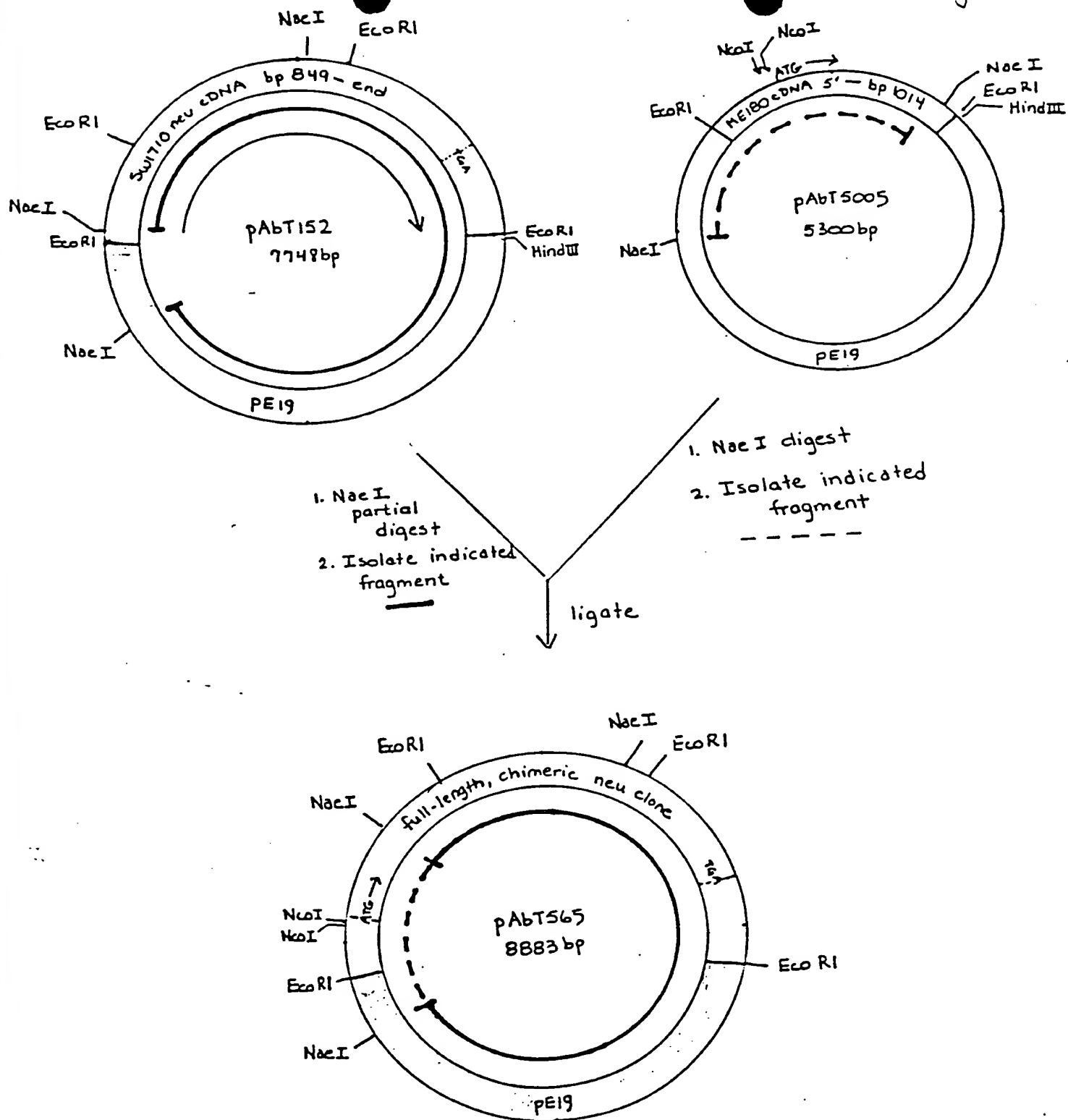
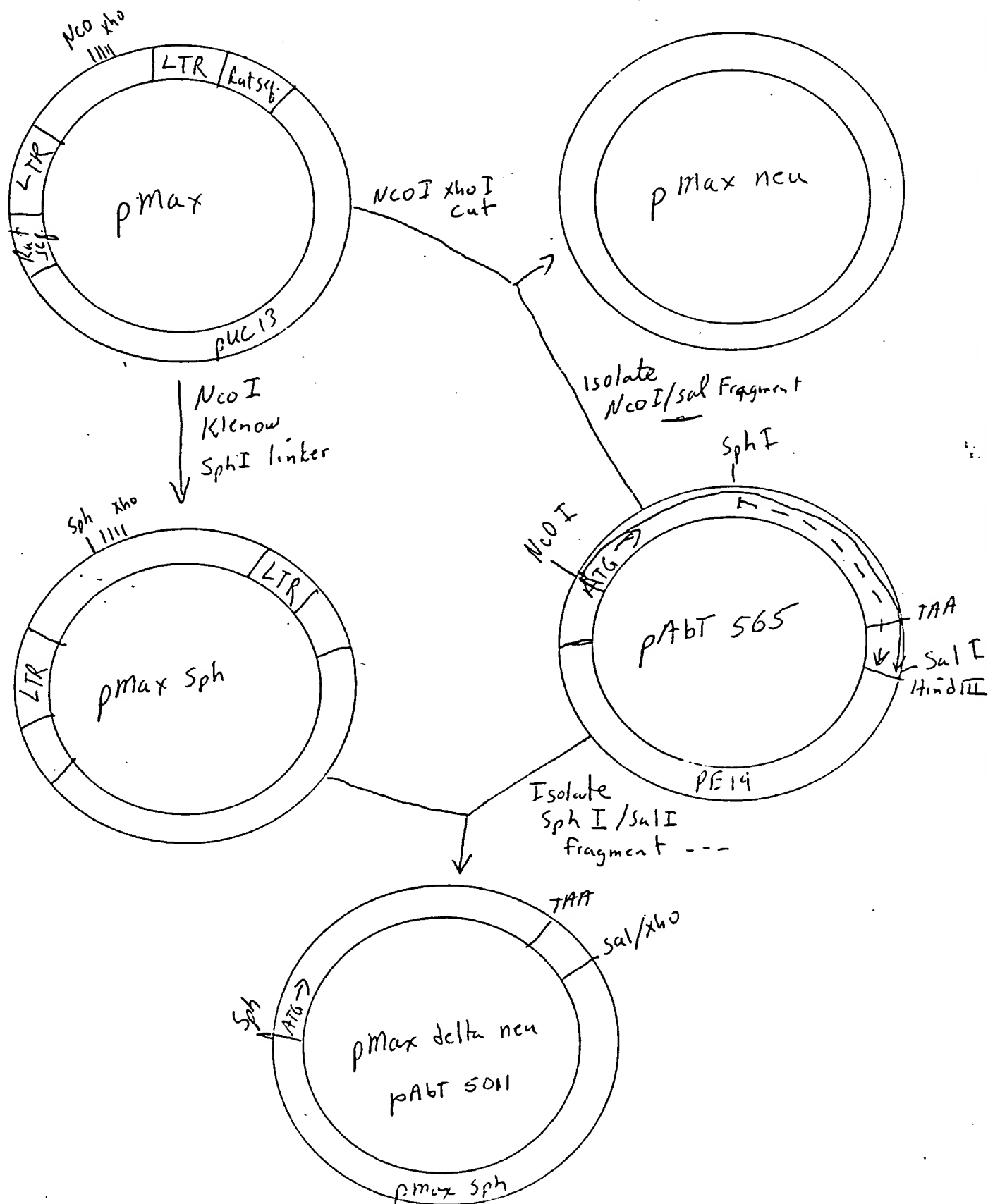
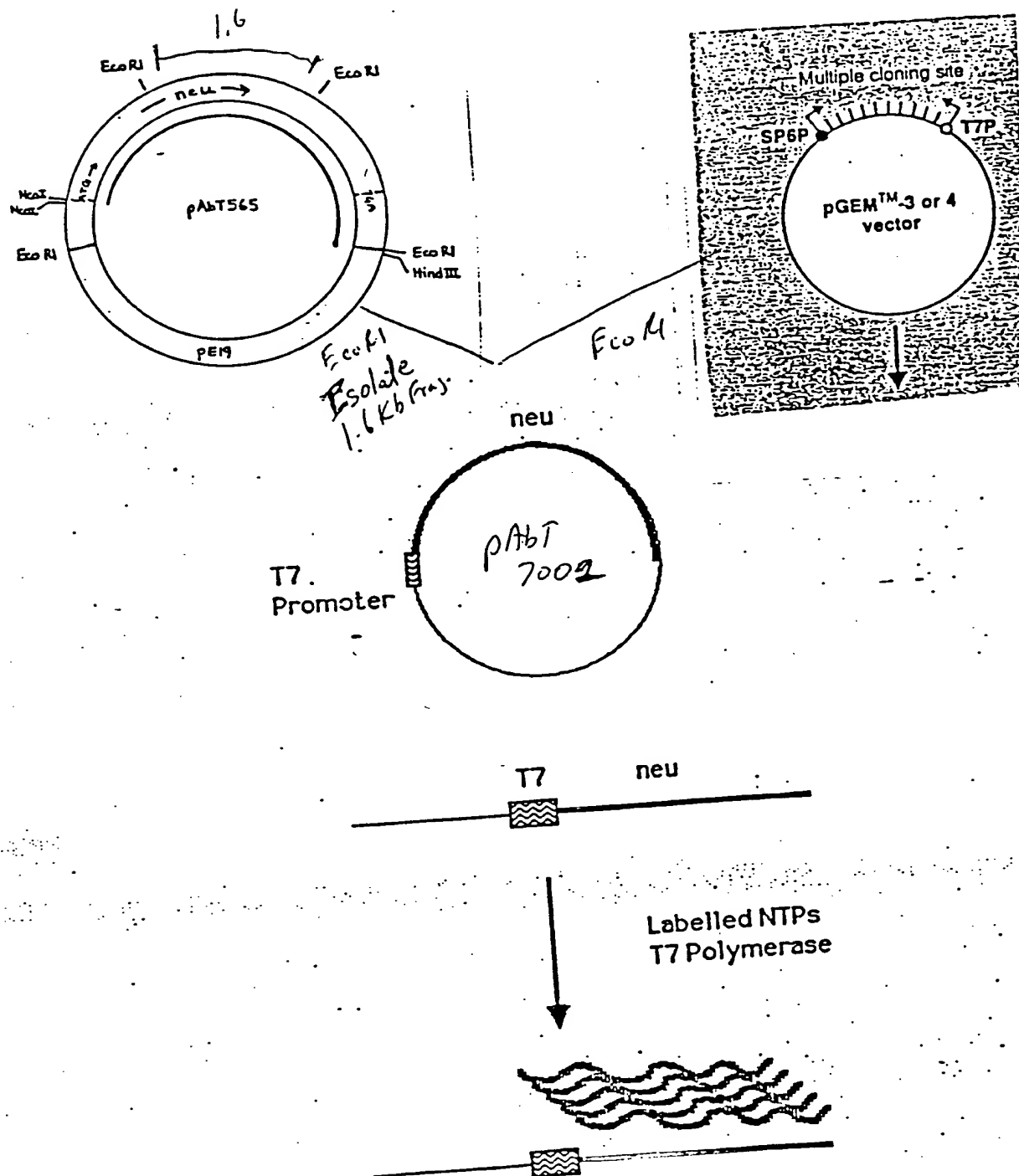
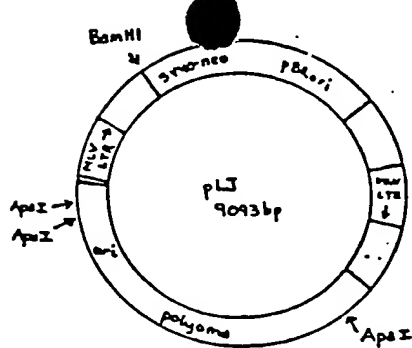


Fig 11. Construction of full length neu cDNA clone from ME180 and SW1710 neu cDNAs

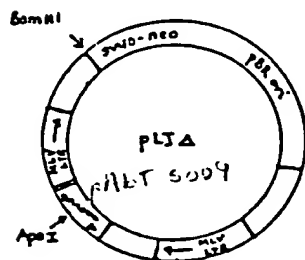


Neu Oncogene Probe Design:

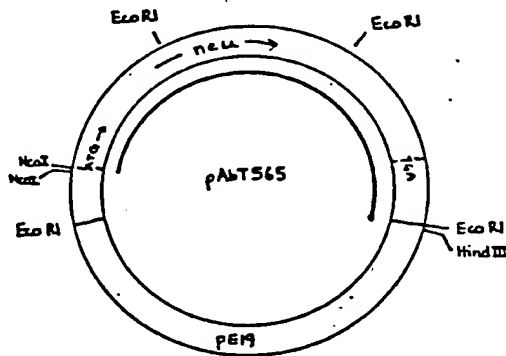




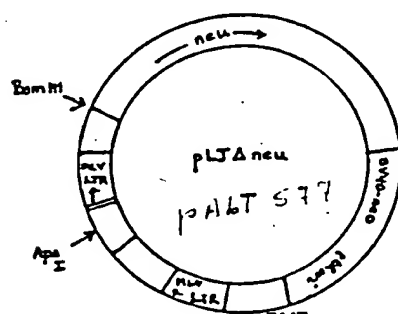
1. ApaI
2. Self ligate



1. BamHI
2. Klenow



1. NeoI-HindIII
2. Klenow
3. Isolate indicated fragment



↓ Calcium phosphate transfection of 3T3 cells

G418^R cell Lines

↓ screen for high neu expression

18-3-7